



PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
Search		Protein	for				Go	Clear
Limits		Preview/Index		History		Clipboard		Details
Display	default	Show:	20	Send to	File	Get Subsequence		

☐ 1: XP\_153478. hypothetical prot...[gi:20909630]

[BLink](#), [Links](#)

LOCUS LOC217730 197 aa linear ROD 17-MAY-2002  
 DEFINITION hypothetical protein XP\_153478 [Mus musculus].  
 ACCESSION XP\_153478  
 VERSION XP\_153478.1 GI:20909630  
 DBSOURCE REFSEQ: accession XM\_153478.1  
 KEYWORDS .  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (residues 1 to 197)  
     AUTHORS NCBI Annotation Project.  
     TITLE Direct Submission  
     JOURNAL Submitted (15-MAY-2002) National Center for Biotechnology  
     Information, NIH, Bethesda, MD 20894, USA  
 COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was  
     predicted from NCBI contig NW\_000053 by automated computational  
     analysis using gene prediction method: GenomeScan.  
     Also see:  
     [Documentation of NCBI's Annotation Process](#)

FEATURES	Location/Qualifiers
source	1..197 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /chromosome="12"
<u>Protein</u>	1..197 /product="hypothetical protein XP_153478"
<u>CDS</u>	1..197 /gene="LOC217730" /coded_by="XM_153478.1:1..594" /db_xref="InterimID:217730"

ORIGIN  
 1 metasaapr vwpfhfafla gflshpeths pgepgplprp pacpsvpfmw vaqwirlifv  
 61 tldvlgsqpm kcpghvalhq dpgpvvrpsg shgnalpldc lmgptshwnv skippfrqps  
 121 kppltdgssq fqgqenpfra cpdfqlgkqm atiakarhpp syilfphpsl snsnavvtln  
 181 rqnlsdssv sissqss  
 //

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[NCBI](#) | [NLM](#) | [NIH](#)

May 26 2003 11:20:12

 **NCBI** *protein-protein* **BLAST**

Nucleotide Protein Translations Retrieve results for an RID

Search

pykwpfhfaffhqilatstiamshcrptvykqtsii  
pykwpfhfaffhqilatstiamshcrptvykqtsii

Set  
subsequence

From:  To:

Choose  
database

nr

Do CD-Search

☐

Now:

**BLAST!**

or

**Reset query**

**Reset all**

### Options for advanced blasting

Limit by entrez  
query

or select from:

(none)



Composition-based  
statistics

☐

Choose filter

☐

Low complexity

☐

Mask for lookup table only

☐

Mask lower case

Expect

20000

Word Size

2



Matrix

PAM30



Gap Costs

Existence: 9 Extension: 1



PSSM

Other advanced

PHI pattern



PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books	
Search		Protein	for					Go	Clear
Limits		Preview/Index		History		Clipboard		Details	
Display	default	Show:	20	Send to	File	Get Subsequence			

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 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (residues 1 to 197)  
 AUTHORS NCBI Annotation Project.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAY-2002) National Center for Biotechnology  
 Information, NIH, Bethesda, MD 20894, USA  
 COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was  
 predicted from NCBI contig NW\_000053 by automated computational  
 analysis using gene prediction method: GenomeScan.  
 Also see:  
[Documentation of NCBI's Annotation Process](#)

FEATURES	Location/Qualifiers
source	1..197 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /chromosome="12"
<u>Protein</u>	1..197 /product="hypothetical protein XP_153478"
<u>CDS</u>	1..197 /gene="LOC217730" /coded_by="XM_153478.1:1..594" /db_xref="InterimID:217730"

ORIGIN

```

1 metasaaprr vwpfhfafla gflshpeths pgepgplprp pacpsvpfmw vaqwirlifv
61 tldvlgsqpm kcpghvalhq dpgpvvrpsg shgnalpldc lmgptshwnv skippfrqps
121 kppltdgssq fqqgenpfra cpdfqlgkqm atiakarhnp syilfphpsl snsnavvtln
181 rqnlsdssv sissqss
//

```

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[NCBI](#) | [NLN](#) | [NIH](#)

May 20 2003 11:20:12



# results of BLAST

search 1

BLASTP 2.2.6 [Apr-09-2003]

## Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053456915-026125-1387

## Query=

(34 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,435,412 sequences; 461,393,641 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

No significant similarity found. For reasons why, [click here](#).

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

Posted date: May 20, 2003 1:52 AM

Number of letters in database: 461,393,641

Number of sequences in database: 1,435,412

Lambda	K	H
0.335	0.141	0.505

## Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 28,353,653

Number of Sequences: 1435412

Number of extensions: 452865

Number of successful extensions: 1347

Number of sequences better than 10.0: 0

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 1347

Number of HSP's gapped (non-prelim): 0

length of query: 34

length of database: 461,393,641

effective HSP length: 10

effective length of query: 24

effective length of database: 447,039,521

effective search space: 10728948504

effective search space used: 10728948504

T: 11

A: 40

X1: 15 ( 7.3 bits)

X2: 38 (14.6 bits)

**results of BLAST****BLASTP 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053457733-016164-25584

**Query=**

(36 letters)

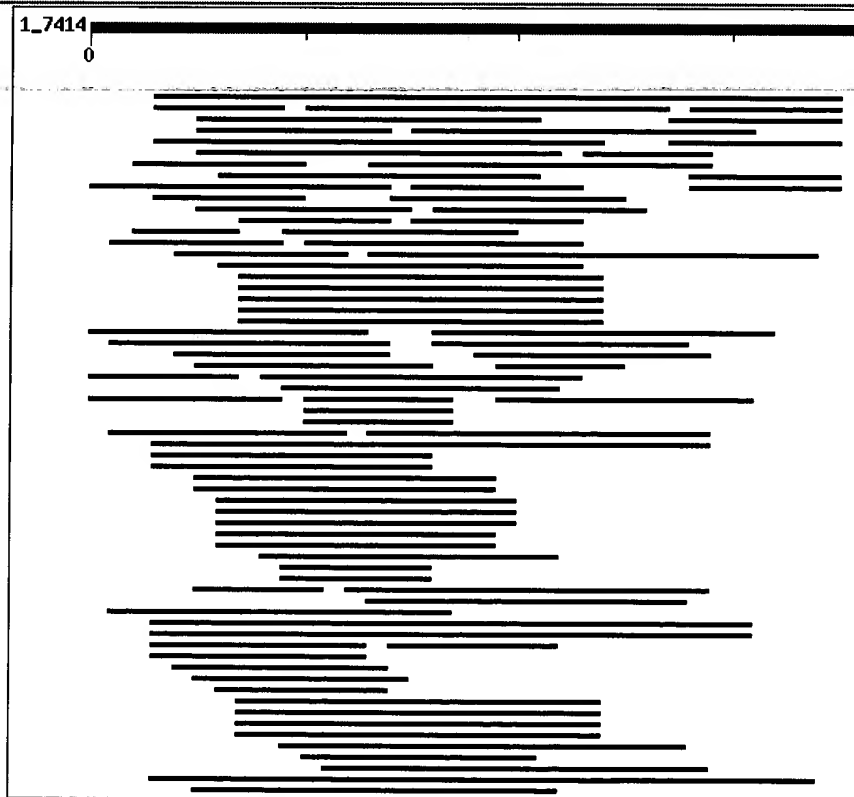
**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF

1,435,412 sequences; 461,393,641 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 100 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

Score E  
(bits) Value

gi 21287767 gb EAA00088.1	ENSANGP00000017962 [Anopheles ga...	31	1.6	
gi 20909630 ref XP_153478.1	hypothetical protein XP_153478...	30	3.8	L
gi 27695175 ref XP_223369.1	similar to low density lipopro...	28	12	L
gi 21242454 ref NP_642036.1	MFS transporter [Xanthomonas a...	28	12	
gi 28900823 ref NP_800478.1	3-hydroxy-3-methylglutaryl CoA...	28	16	
gi 30177923 gb EAA45104.1	ENSANGP00000023294 [Anopheles ga...	28	16	
gi 21231138 ref NP_637055.1	MFS transporter [Xanthomonas c...	28	16	
gi 23137395 ref ZP_00119101.1	hypothetical protein [Cytoph...	27	22	
gi 21245069 ref NP_644651.1	conserved hypothetical protein...	27	22	
gi 24374681 ref NP_718724.1	DnaJ domain protein [Shewanell...	27	30	
gi 18398283 ref NP_565400.1	F-box protein family, AtFBL10 ...	27	30	
gi 10946860 ref NP_067441.1	TATA box binding protein (Tbp)...	27	30	L
gi 18462766 gb AAL72538.1	hypothetical protein [Shigella f...	27	30	
gi 27672343 ref XP_221755.1	similar to hypothetical protei...	27	30	L
gi 28871387 ref NP_794006.1	hypothetical protein [Pseudomo...	27	30	
gi 23128861 ref ZP_00110699.1	hypothetical protein [Nostoc...	27	30	
gi 21293138 gb EAA05283.1	ENSANGP00000008298 [Anopheles ga...	27	40	
gi 9801567 gb AAF97943.2	cytochrome P450 CYP6N4v3 [Aedes a...	27	40	
gi 9801568 gb AAF97944.2	cytochrome P450 CYP6N4v4 [Aedes a...	27	40	
gi 9801569 gb AAF97945.2	cytochrome P450 CYP6N4v5 [Aedes a...	27	40	
gi 28564982 gb AAO38684.1	truncated PDR5 [Saccharomyces kl...	27	40	
gi 15078968 ref NP_149719.1	256R [Invertebrate iridescent ...	27	40	
gi 15641102 ref NP_230734.1	periplasmic binding protein-re...	27	40	
gi 19114288 ref NP_593376.1	hypothetical protein [Schizosa...	27	40	
gi 9801570 gb AAF97946.2	cytochrome P450 CYP6N4v6 [Aedes a...	27	40	
gi 9801564 gb AAF97940.2	cytochrome P450 CYP6N4v1 [Aedes a...	27	40	
gi 729930 sp P16270 LECN_PEA	NONSEED LECTIN PRECURSOR >gi 3...	26	53	
gi 30260580 ref NP_842957.1	hypothetical protein [Bacillus...	26	53	
gi 22293495 emb CAD31853.1	putative chemosensory receptor ...	26	53	
gi 26987557 ref NP_742982.1	conserved hypothetical protein...	26	53	
gi 30023459 ref NP_835090.1	Beta-1,3-N-acetylglucosaminylt...	26	53	
gi 17230565 ref NP_487113.1	probable glycosyl transferase ...	26	53	
gi 27500354 ref XP_211309.1	hypothetical protein XP_211309...	26	53	L
gi 13812138 ref NP_113265.1	chromosomal region maintenance...	26	53	
gi 27706584 ref XP_242294.1	hypothetical protein XP_242294...	26	53	L
gi 100052 pir S20988	lectin - garden pea >gi 169172 gb AAA...	26	53	
gi 7510844 pir T29765	hypothetical protein ZC581.4 - Caeno...	26	53	
gi 21398366 ref NP_654351.1	hypothetical protein predicted...	26	53	
gi 5579428 gb AAD45549.1 U70376_14	Spce [Streptomyces netro...	26	53	
gi 630666 pir S40748	hypothetical protein F54C8.6 - Caenor...	26	72	
gi 28917410 gb EAA27114.1	hypothetical protein [Neurospora...	26	72	
gi 23612355 ref NP_703935.1	transportin [Plasmodium falcip...	26	72	
gi 15802965 ref NP_288995.1	Z3699 gene product [Escherichi...	26	72	
gi 16130359 ref NP_416929.1	orf, hypothetical protein [Esc...	26	72	
gi 17297993 dbj BAB78507.1	transportin [Plasmodium falcipa...	26	72	
gi 19113394 ref NP_596602.1	SNF2 family dna repair protein...	26	72	
gi 13476001 ref NP_107571.1	ABC transporter, substrate bin...	26	72	
gi 30020491 ref NP_832122.1	hypothetical protein [Bacillus...	26	72	
gi 22298512 ref NP_681759.1	ORF_ID:tlr0969-probable membra...	26	72	
gi 21292670 gb EAA04815.1	ENSANGP00000019532 [Anopheles ga...	26	72	
gi 23059042 ref ZP_00084044.1	hypothetical protein [Pseudo...	26	72	
gi 15964592 ref NP_384945.1	PROBABLE RIBONUCLEASE HII PROT...	26	72	
gi 28901509 ref NP_801164.1	putative ferrichrome ABC trans...	26	72	
gi 17553568 ref NP_499077.1	Predicted CDS, putative membra...	26	72	L
gi 15240890 ref NP_195730.1	expressed protein [Arabidopsis...	26	72	
gi 15889786 ref NP_355467.1	AGR_C_4580p [Agrobacterium tum...	26	72	
gi 23307111 dbj BAC16541.1	ferric vibrioferrin transport s...	26	72	
gi 30176975 gb EAA08960.2	ENSANGP00000019639 [Anopheles ga...	26	72	
gi 18860525 ref NP_573365.1	CG7876-PA [Drosophila melanoga...	26	72	L
gi 27753111 emb CAA84735.2	C. elegans SRG-11 protein (corr...	26	72	

gi 25342678 pir B88555	protein F54C8.6 [imported] - Caenor...	26	72	
gi 30157001 ref XP_291865.2	similar to olfactory receptor ...	25	96	L
gi 27707330 ref XP_242328.1	hypothetical protein XP_242328...	25	96	L
gi 15611696 ref NP_223347.1	putative TYPE II DNA MODIFICAT...	25	96	
gi 15217347 gb AAK92685.1 AC090714.18	putative retrotranspo...	25	96	
gi 630612 pir S44629	F22B7.10 protein - Caenorhabditis ele...	25	96	
gi 16944534 emb CAD11330.1	hypothetical protein [Neurospor...	25	96	
gi 30179202 gb EAA45649.1	ENSANGP00000024832 [Anopheles ga...	25	96	
gi 27685447 ref XP_217453.1	serine (or cysteine) proteinas...	25	96	L
gi 1477386 gb AAC37338.1	This CDS feature is included to s...	25	96	
gi 24666563 ref NP_649079.2	CG6836-PA [Drosophila melanoga...	25	96	L
gi 17861760 gb AAL39357.1	GH26215p [Drosophila melanogaster]	25	96	L
gi 121111 sp P07092 GDN RAT	Glia derived nexin precursor (G...	25	96	L
gi 30179203 gb EAA45650.1	ENSANGP00000025224 [Anopheles ga...	25	96	
gi 15232200 ref NP_186830.1	expressed protein [Arabidopsis...	25	96	
gi 13660729 gb AAK32960.1	cytochrome P450 [Anopheles gambiae]	25	96	
gi 28515296 ref XP_288452.1	hypothetical protein XP_288452...	25	96	L
gi 26336525 dbj BAC31945.1	unnamed protein product [Mus mu...	25	96	L
gi 30840221 emb CAD61285.1	fertility restorer [Raphanus sa...	25	96	
gi 17552842 ref NP_498909.1	Dumpy : shorter than wild-type...	25	96	L
gi 30179201 gb EAA45648.1	ENSANGP00000025060 [Anopheles ga...	25	96	
gi 20837204 ref XP_158536.1	hypothetical protein XP_158536...	25	129	L
gi 29349732 ref NP_813235.1	conserved hypothetical protein...	25	129	
gi 15131119 emb CAC48190.1	NADH dehydrogenase subunit 2 [L...	25	129	
gi 23273294 gb AAH34950.1	TANK-binding kinase 1 [Homo sapi...	25	129	L
gi 7019547 ref NP_037386.1	TANK-binding kinase 1; NF-kB-ac...	25	129	L
gi 23058842 ref ZP_00083865.1	hypothetical protein [Pseudo...	25	129	
gi 26991318 ref NP_746743.1	conserved hypothetical protein...	25	129	
gi 23042124 ref ZP_00073532.1	hypothetical protein [Tricho...	25	129	
gi 15791673 ref NP_281496.1	hypothetical protein Cj0305c [...	25	129	
gi 26655514 gb AAN85858.1	NADH dehydrogenase subunit II [M...	25	129	
gi 14276199 gb AAK58140.1	NADH dehydrogenase subunit II [M...	25	129	
gi 14276231 gb AAK58156.1	NADH dehydrogenase subunit II [B...	25	129	
gi 22957373 gb ZP_00005078.1	hypothetical protein [Rhodoba...	25	129	
gi 17543364 ref NP_501353.1	Putative nuclear protein, with...	25	129	L
gi 15601658 ref NP_233289.1	permease [Vibrio cholerae] >gi...	25	129	
gi 27718495 ref XP_216902.1	similar to TANK-binding kinase...	25	129	L
gi 21347201 gb AAL50224.1	NADH dehydrogenase subunit II [M...	24	173	
gi 15800733 ref NP_286747.1	unknown [Escherichia coli O157...	24	173	
gi 17456139 ref XP_051362.2	similar to Transmembrane 6 sup...	24	173	L

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|21287767|gb|EAA00088.1| ENSANGP00000017962 [Anopheles gambiae str. PEST]  
Length = 314

Score = 31.2 bits (66), Expect = 1.6

Identities = 19/47 (40%), Positives = 23/47 (48%), Gaps = 18/47 (38%)

Query: 4 WPFHFAFFH----Q-----ILATSTI--AMSHCRPTVYKQTSII 36

WP+H A FH Q IL +TI A SHC VY Q+ +I

Sbjct: 52 WPHVALFHRKDAQYAYACGGSILDENTILTA-SHC---VYTQSGVI 94

☐ >gi|20909630|ref|XP\_153478.1| hypothetical protein XP\_153478 [Mus musculus]  
Length = 197

Score = 29.9 bits (63), Expect = 3.8

Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 4 WPFHFHAF 10  
 WPFHFHAF  
 Sbjct: 12 WPFHFHAF 18

☐ >gi|27695175|ref|XP\_223369.1| similar to low density lipoprotein receptor-relat  
 low density lipoprotein-related protein 4; Low Density  
 Lipoprotein Receptor Related Protein 4; corin [Mus  
 musculus] [Rattus norvegicus]  
 Length = 276

Score = 28.2 bits (59), Expect = 12  
 Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 6 FHFAFFHQIL 15  
 FHF+ FHQ+L  
 Sbjct: 2 FHFSLFHQVL 11

☐ >gi|21242454|ref|NP\_642036.1| MFS transporter [Xanthomonas axonopodis pv. citri  
 gi|21107899|gb|AAM36572.1| MFS transporter [Xanthomonas axonopodis pv. citri str.  
 Length = 474

Score = 28.2 bits (59), Expect = 12  
 Identities = 10/17 (58%), Positives = 12/17 (70%)

Query: 6 FHFAFFHQILATSTIAM 22  
 F FAFF Q LA T+A+  
 Sbjct: 167 FAFAFFVQFLAVPTVAL 183

☐ >gi|28900823|ref|NP\_800478.1| 3-hydroxy-3-methylglutaryl CoA reductase [Vibrio p  
 RIMD 2210633]  
 gi|28809269|dbj|BAC62311.1| 3-hydroxy-3-methylglutaryl CoA reductase [Vibrio para  
 Length = 420

Score = 27.8 bits (58), Expect = 16  
 Identities = 10/18 (55%), Positives = 11/18 (61%), Gaps = 5/18 (27%)

Query: 11 FHQILATSTIAMSHCRPT 28  
 FH ILATS I +PT  
 Sbjct: 225 FHHILATSPI-----KPT 237

☐ >gi|30177923|gb|EAA45104.1| ENSANGP00000023294 [Anopheles gambiae str. PEST]  
 Length = 232

Score = 27.8 bits (58), Expect = 16  
 Identities = 15/36 (41%), Positives = 17/36 (47%), Gaps = 15/36 (41%)

Query: 4 WPFHFHFAFFHQ-----ILATSTI--AMSHC 25  
 WP+H A FHQ IL +TI A SHC  
 Sbjct: 1 WPWHAAIFHQDKHKEYACGGSILDETTILTA-SHC 35

☐ >gi|21231138|ref|NP\_637055.1| MFS transporter [Xanthomonas campestris pv. campes  
 33913]  
 gi|21112775|gb|AAM40979.1| MFS transporter [Xanthomonas campestris pv. campestris  
 33913]  
 Length = 468

Score = 27.8 bits (58), Expect = 16  
 Identities = 10/18 (55%), Positives = 13/18 (72%)

Query: 6 FHFAFFHQILATSTIAMS 23  
 F FAFF Q LA ++A+S  
 Sbjct: 166 FAFAFFLQFLAVPSVALS 183



☐ >[gi|23137395|ref|ZP\\_00119101.1|](#) hypothetical protein [Cytophaga hutchinsonii]  
Length = 414

Score = 27.4 bits (57), Expect = 22  
Identities = 13/35 (37%), Positives = 16/35 (45%), Gaps = 19/35 (54%)

Query: 7 HF---AFF-----HQIL-----ATSTIAM 22  
HF AFF H++L +TSTIAM  
Sbjct: 264 HPVIGAFFGAMLLSHELLGKENFHIVEKSTSTIAM 298

☐ >[gi|21245069|ref|NP\\_644651.1|](#) conserved hypothetical protein [Xanthomonas axonop  
str. 306]  
[gi|21110802|gb|AAM39187.1|](#) conserved hypothetical protein [Xanthomonas axonopodis  
str. 306]  
Length = 129

Score = 27.4 bits (57), Expect = 22  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 3 KWPFHFAFF 11  
KW F FFAFF  
Sbjct: 12 KWQFRFAFF 20

☐ >[gi|24374681|ref|NP\\_718724.1|](#) DnaJ domain protein [Shewanella oneidensis MR-1]  
[gi|24349326|gb|AAN56168.1|AE015754.2](#) DnaJ domain protein [Shewanella oneidensis M  
Length = 402

Score = 26.9 bits (56), Expect = 30  
Identities = 9/11 (81%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 6 FHFAFFHQILA 16  
FH AFF QILA  
Sbjct: 170 FH-AFFEQILA 179

☐ >[gi|18398283|ref|NP\\_565400.1|](#) F-box protein family, AtFBL10 [Arabidopsis thaliana  
[gi|25372906|pir|B84547](#) hypothetical protein At2g17020 [imported] - Arabidopsis t  
[gi|13605809|gb|AAK32890.1|AF367303.1](#) At2g17020 [Arabidopsis thaliana]  
[gi|22137200|gb|AAM91445.1|](#) At2g17020/At2g17020 [Arabidopsis thaliana]  
Length = 656

Score = 26.9 bits (56), Expect = 30  
Identities = 9/14 (64%), Positives = 12/14 (85%), Gaps = 1/14 (7%)

Query: 11 FHQILATSTIAMSH 24  
FH ILAT T+++SH  
Sbjct: 370 FHDILAT-TLSLSH 382

☐ >[gi|10946860|ref|NP\\_067441.1|](#) TATA box binding protein (Tbp)-associated factor,  
A [Mus musculus]  
[gi|1842204|emb|CAA71091.1|](#) TAFI48 protein [Mus musculus]  
Length = 453

Score = 26.9 bits (56), Expect = 30  
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 4 WP-FHFAFF 11  
WP FHF+FF  
Sbjct: 380 WPAFHFSFF 388

☐ >[gi|18462766|gb|AAL72538.1|](#) hypothetical protein [Shigella flexneri 2a]  
Length = 139

Score = 26.9 bits (56), Expect = 30

Identities = 11/17 (64%), Positives = 13/17 (76%), Gaps = 2/17 (11%)

Query: 14 ILATSTIAMSHCRPTVY 30  
ILA+S I+M H R TVY  
Sbjct: 87 ILASSKISMLH-R-TVY 101

☐ >[gi|27672343|ref|XP\\_221755.1|](#) similar to hypothetical protein MGC2408 [Homo sap  
norvegicus]  
Length = 256

Score = 26.9 bits (56), Expect = 30  
Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 2/16 (12%)

Query: 1 PYKWPF-HFAFFHQIL 15  
PY+W F FAFHH +L  
Sbjct: 130 PYEW-FGDFAFHHALL 144

☐ >[gi|28871387|ref|NP\\_794006.1|](#) hypothetical protein [Pseudomonas syringae pv. tom  
[gi|28854638|gb|AA057701.1|](#) hypothetical protein [Pseudomonas syringae pv. tomato]  
Length = 1111

Score = 26.9 bits (56), Expect = 30  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 8 FAFHHQIL 15  
FAFHHQ+L  
Sbjct: 728 FAFHHQLL 735

☐ >[gi|23128861|ref|ZP\\_00110699.1|](#) hypothetical protein [Nostoc punctiforme]  
Length = 2181

Score = 26.9 bits (56), Expect = 30  
Identities = 8/12 (66%), Positives = 8/12 (66%)

Query: 10 FFHQILATSTIA 21  
FFH I A TIA  
Sbjct: 595 FFHHIFANPTIA 606

☐ >[gi|21293138|gb|EAA05283.1|](#) ENSANGP00000008298 [Anopheles gambiae str. PEST]  
Length = 602

Score = 26.5 bits (55), Expect = 40  
Identities = 8/12 (66%), Positives = 9/12 (75%)

Query: 15 LATSTIAMSHCR 26  
L TSTI + HCR  
Sbjct: 580 LVTSTIVLEHCR 591

☐ >[gi|9801567|gb|AAF97943.2|](#) cytochrome P450 CYP6N4v3 [Aedes albopictus]  
Length = 216

Score = 26.5 bits (55), Expect = 40  
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFHHQILA---TSTIAMSHC 25  
F FF LA TS+ AMS+C  
Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >[gi|9801568|gb|AAF97944.2|](#) cytochrome P450 CYP6N4v4 [Aedes albopictus]  
Length = 216

Score = 26.5 bits (55), Expect = 40  
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25  
 F FF LA TS+ AMS+C  
 Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >[gi|9801569|gb|AAF97945.2|](#) cytochrome P450 CYP6N4v5 [Aedes albopictus]  
 Length = 216

Score = 26.5 bits (55), Expect = 40  
 Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25  
 F FF LA TS+ AMS+C  
 Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >[gi|28564982|gb|AAO38684.1|](#) truncated PDR5 [Saccharomyces kluyveri]  
 Length = 1023

Score = 26.5 bits (55), Expect = 40  
 Identities = 12/20 (60%), Positives = 13/20 (65%), Gaps = 4/20 (20%)

Query: 7 HFAFFHQILA--TSTIAMSH 24  
 HF FF+ L TST AMSH  
 Sbjct: 639 HF-FFY-FLVSVTSTFAMSH 656

☐ >[gi|15078968|ref|NP\\_149719.1|](#) 256R [Invertebrate iridescent virus 6]  
[gi|15042337|gb|AAK82117.1|AF303741](#) 256R [Chilo iridescent virus]  
 Length = 78

Score = 26.5 bits (55), Expect = 40  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 YKWPFHF 10  
 ++W FHF  
 Sbjct: 39 FRWSFHF 47

☐ >[gi|15641102|ref|NP\\_230734.1|](#) periplasmic binding protein-related protein [Vibri  
[gi|11345643|pir|A82245](#) periplasmic binding protein-related protein VC1089 [impor  
 Vibrio cholerae (strain N16961 serogroup O1)  
[gi|9655557|gb|AAF94248.1|](#) periplasmic binding protein-related protein [Vibrio cho  
 Length = 270

Score = 26.5 bits (55), Expect = 40  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 5 PFHF 13  
 P+H+ FFH  
 Sbjct: 80 PYHYTFFH 88

☐ >[gi|19114288|ref|NP\\_593376.1|](#) hypothetical protein [Schizosaccharomyces pombe]  
[gi|3219957|sp|P87136|YDM5](#) SCHPO Hypothetical protein C57A7.05 in chromosome I  
[gi|7491179|pir|T38949](#) hypothetical protein SPAC57A7.05 - fission yeast  
 (Schizosaccharomyces pombe)  
[gi|2104440|emb|CAB08763.1|](#) hypothetical protein; similar to S. cerevisiae YDL231C  
 contains 11 predicted transmembrane helices;  
 leucine-serine rich [Schizosaccharomyces pombe]  
 Length = 1337

Score = 26.5 bits (55), Expect = 40  
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 3 KWPFHF 8  
 KWPFHF  
 Sbjct: 1308 KWPFHF 1313

☐ >gi|9801570|gb|AAF97946.2| cytochrome P450 CYP6N4v6 [*Aedes albopictus*]  
Length = 216

Score = 26.5 bits (55), Expect = 40  
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25  
F FF LA TS+ AMS+C  
Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >gi|9801564|gb|AAF97940.2| cytochrome P450 CYP6N4v1 [*Aedes albopictus*]  
Length = 435

Score = 26.5 bits (55), Expect = 40  
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25  
F FF LA TS+ AMS+C  
Sbjct: 299 FVFF---LAGFETSSTAMSYC 316

☐ >gi|729930|sp|P16270|LECN\_PEA NONSEED LECTIN PRECURSOR  
gi|309675|gb|AAA33675.1| lectin  
Length = 265

Score = 26.1 bits (54), Expect = 53  
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 16 ATSTIAMSH 24  
ATSTIA+SH  
Sbjct: 235 ATSTIAVSH 243

☐ >gi|30260580|ref|NP\_842957.1| hypothetical protein [*Bacillus anthracis* str. Ames]  
gi|30253948|gb|AAP24443.1| hypothetical protein [*Bacillus anthracis* str. Ames]  
Length = 920

Score = 26.1 bits (54), Expect = 53  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 11 FHQILATS 18  
FHQI+ATS  
Sbjct: 439 FHQIMATS 446

☐ >gi|22293495|emb|CAD31853.1| putative chemosensory receptor 7 [*Heliothis viresce*]  
Length = 397

Score = 26.1 bits (54), Expect = 53  
Identities = 10/17 (58%), Positives = 11/17 (64%), Gaps = 5/17 (29%)

Query: 1 PY--K-WPFHFAFFHQI 14  
PY K WPF A+ HQI  
Sbjct: 174 PYELKYWPF--AYIHQI 188

☐ >gi|26987557|ref|NP\_742982.1| conserved hypothetical protein [*Pseudomonas putida*]  
gi|24982231|gb|AAN66446.1|AE016274\_3 conserved hypothetical protein [*Pseudomonas*]  
Length = 136

Score = 26.1 bits (54), Expect = 53  
Identities = 12/30 (40%), Positives = 14/30 (46%), Gaps = 15/30 (50%)

Query: 16 ATSTIAMSHC-----RPTVYKQ 32  
A+ST+AMS C R VYKQ  
Sbjct: 42 ASSTVAMSACIGAETQVQDQRLNR--VYKQ 69

☐ >gi|30023459|ref|NP\_835090.1| Beta-1,3-N-acetylglucosaminyltransferase [Bacillus  
14579]  
gi|29899020|gb|AAP12291.1| Beta-1,3-N-acetylglucosaminyltransferase [Bacillus cer  
14579]  
Length = 326

Score = 26.1 bits (54), Expect = 53  
Identities = 12/24 (50%), Positives = 15/24 (62%), Gaps = 8/24 (33%)

Query: 9 AFF-HQILA-TST-----IAMSH 24  
AF HQ++A TST IAM+H  
Sbjct: 148 AFLTHQVVAQTSTWIFKRSIAMNH 171

☐ >gi|17230565|ref|NP\_487113.1| probable glycosyl transferase [Nostoc sp. PCC 7120  
gi|25530026|pir|AB2190 hypothetical protein alr3073 [imported] - Nostoc sp. (str  
7120)  
gi|17132167|dbj|BAB74772.1| ORF\_ID:alr3073~probable glycosyl transferase [Nostoc  
Length = 324

Score = 26.1 bits (54), Expect = 53  
Identities = 9/18 (50%), Positives = 9/18 (50%), Gaps = 8/18 (44%)

Query: 2 YKWPF---HFAPFHQIL 15  
YKWPF HQIL  
Sbjct: 185 YKWPFVVVKQ---HQIL 198

☐ >gi|27500354|ref|XP\_211309.1| hypothetical protein XP\_211309 [Homo sapiens]  
Length = 132

Score = 26.1 bits (54), Expect = 53  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 11 FHQILATS 18  
FHQIL+TS  
Sbjct: 61 FHQILSTS 68

☐ >gi|13812138|ref|NP\_113265.1| chromosomal region maintenance protein CRM1 [Guill  
gi|25396709|pir|F90086 chromosomal region maintenance protein CRM1 [imported] -  
theta nucleomorph  
gi|13794450|gb|AAK39825.1|AF165818 33 chromosomal region maintenance protein CRM1  
Length = 949

Score = 26.1 bits (54), Expect = 53  
Identities = 10/15 (66%), Positives = 11/15 (73%), Gaps = 1/15 (6%)

Query: 10 FFHQILAT-STIAMS 23  
FFH+IL STI MS  
Sbjct: 358 FFHKILINLSTILMS 372

☐ >gi|27706584|ref|XP\_242294.1| hypothetical protein XP\_242294 [Rattus norvegicus]  
Length = 415

Score = 26.1 bits (54), Expect = 53  
Identities = 8/11 (72%), Positives = 10/11 (90%), Gaps = 1/11 (9%)

Query: 17 TSTIAMSHCRP 27  
TS +AMS+CRP  
Sbjct: 338 TS-VAMSNCRP 347

☐ >gi|100052|pir|S20988 lectin - garden pea  
gi|169172|gb|AAA33691.1| vegetative lectin  
Length = 265

Score = 26.1 bits (54), Expect = 53

Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 16 ATSTIAMSH 24  
ATSTIA+SH  
Sbjct: 235 ATSTIAVSH 243

☐ >[gi|7510844|pir|T29765](#) hypothetical protein ZC581.4 - *Caenorhabditis elegans*  
Length = 209

Score = 26.1 bits (54), Expect = 53  
Identities = 9/15 (60%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query: 5 PFHF--AFFHQ--IL 15  
PFHF FF Q IL  
Sbjct: 57 PFHFPQTFFQQPHIL 71

☐ >[gi|21398366|ref|NP\\_654351.1|A2012](#) hypothetical protein predicted by GeneMark [*Bacill*]  
Length = 920

Score = 26.1 bits (54), Expect = 53  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 11 FHQILATS 18  
FHQI+ATS  
Sbjct: 439 FHQIMATS 446

☐ >[gi|5579428|gb|AAD45549.1|U70376\\_14](#) SpcE [*Streptomyces netropsis*]  
Length = 427

Score = 26.1 bits (54), Expect = 53  
Identities = 10/15 (66%), Positives = 11/15 (73%), Gaps = 3/15 (20%)

Query: 6 FH--FAFFHQ-ILAT 17  
FH FAF HQ +LAT  
Sbjct: 391 FHTCFAFLHQALLAT 405

☐ >[gi|630666|pir|S40748](#) hypothetical protein F54C8.6 - *Caenorhabditis elegans*  
Length = 309

Score = 25.7 bits (53), Expect = 72  
Identities = 11/22 (50%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 7 HFA--FFHQ----ILAT-STIA 21  
HF FFHQ IL++ +TIA  
Sbjct: 223 HFVVQFFHQIHLILSSIATIA 244

☐ >[gi|28917410|gb|EAA27114.1|](#) hypothetical protein [*Neurospora crassa*]  
Length = 620

Score = 25.7 bits (53), Expect = 72  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 1 PYKWPFHF 8  
PYKW F F  
Sbjct: 36 PYKWTFQF 43

☐ >[gi|23612355|ref|NP\\_703935.1|](#) transportin [*Plasmodium falciparum* 3D7]  
[gi|23498596|emb|CAD50547.1|](#) transportin [*Plasmodium falciparum* 3D7]  
Length = 1147

Score = 25.7 bits (53), Expect = 72  
Identities = 7/8 (87%), Positives = 7/8 (87%)

**results of BLAST****BLASTP 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053457234-04130-17010

search 2

**Query=**

(34 letters)

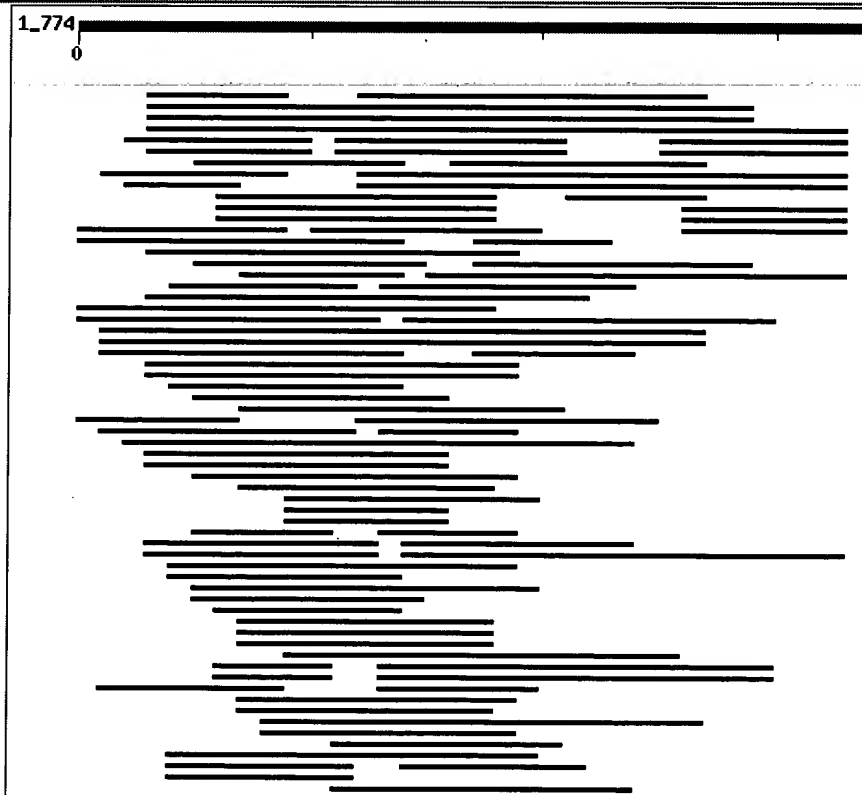
**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF

1,435,412 sequences; 461,393,641 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 101 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

gi	20909630	ref	XP_153478.1	hypothetical protein XP_153478...	30	3.8	L
gi	19113394	ref	NP_596602.1	SNF2 family dna repair protein...	30	3.8	
gi	27685447	ref	XP_217453.1	serine (or cysteine) proteinase...	29	5.1	L
gi	121111	sp	P07092 GDN_RAT	Glia derived nexin precursor (G...	29	5.1	L
gi	21287767	gb	EAA00088.1	ENSANGP00000017962 [Anopheles ga...	29	6.9	
gi	25148238	ref	NP_499962.2	Protein kinase family member (...)	29	9.2	
gi	7505805	pir	T34435	hypothetical protein K11H12.9 - Caen...	29	9.2	
gi	27695175	ref	XP_223369.1	similar to low density lipopro...	28	12	L
gi	17558564	ref	NP_506763.1	Predicted CDS, putative plasma...	28	12	L
gi	30145805	emb	CAB02832.2	C. elegans SRW-24 protein (corr...	28	12	
gi	630666	pir	S40748	hypothetical protein F54C8.6 - Caenor...	28	17	
gi	17555608	ref	NP_498145.1	Predicted CDS, putative membra...	28	17	L
gi	17553568	ref	NP_499077.1	Predicted CDS, putative membra...	28	17	L
gi	25342678	pir	B88555	protein F54C8.6 [imported] - Caenor...	28	17	
gi	21245069	ref	NP_644651.1	conserved hypothetical protein...	27	22	
gi	24374681	ref	NP_718724.1	DnaJ domain protein [Shewanell...	27	30	
gi	10946860	ref	NP_067441.1	TATA box binding protein (Tbp)...	27	30	L
gi	27672343	ref	XP_221755.1	similar to hypothetical protei...	27	30	L
gi	28871387	ref	NP_794006.1	hypothetical protein [Pseudomo...	27	30	
gi	20094540	ref	NP_614387.1	Uncharacterized membrane prote...	27	30	
gi	9632199	ref	NP_048911.1	a555R [Paramecium bursaria Chlo...	27	30	
gi	15078968	ref	NP_149719.1	256R [Invertebrate iridescent ...]	27	40	
gi	30177923	gb	EAA45104.1	ENSANGP00000023294 [Anopheles ga...	27	40	
gi	15641102	ref	NP_230734.1	periplasmic binding protein-re...	27	40	
gi	19114288	ref	NP_593376.1	hypothetical protein [Schizosa...	27	40	
gi	22293495	emb	CAD31853.1	putative chemosensory receptor ...	26	54	
gi	17230565	ref	NP_487113.1	probable glycosyl transferase ...	26	54	
gi	19552310	ref	NP_600312.1	hypothetical membrane protein ...	26	54	
gi	22982800	ref	ZP_00028030.1	hypothetical protein [Burkho...	26	54	
gi	14521448	ref	NP_126924.1	CARBON STARVATION PROTEIN A. [...]	26	54	
gi	17544706	ref	NP_501719.1	3-oxo-5-alpha-steroid 4-dehydr...	26	54	L
gi	7510844	pir	T29765	hypothetical protein ZC581.4 - Caeno...	26	54	
gi	15235511	ref	NP_195444.1	ATPase, E1-E2 type family [Ara...	26	54	
gi	5579428	gb	AAD45549.1	U70376_14 SpcE [Streptomyces netro...	26	54	
gi	7710954	emb	CAB90352.1	putative metal ATPase [Arabidops...	26	54	
gi	15606525	ref	NP_213905.1	NADH dehydrogenase I chain M [...]	26	54	
gi	21242454	ref	NP_642036.1	MFS transporter [Xanthomonas a...	26	72	
gi	28917410	gb	EAA27114.1	hypothetical protein [Neurospora...	26	72	
gi	23612355	ref	NP_703935.1	transportin [Plasmodium falcip...	26	72	
gi	17297993	dbj	BAB78507.1	transportin [Plasmodium falcipa...	26	72	
gi	30177001	gb	EAA08763.2	ENSANGP00000021306 [Anopheles ga...	26	72	
gi	27366492	ref	NP_762019.1	Cation/multidrug efflux pump [...]	26	72	
gi	15903492	ref	NP_359042.1	Conserved hypothetical protein...	26	72	
gi	13812138	ref	NP_113265.1	chromosomal region maintenance...	26	72	
gi	13476001	ref	NP_107571.1	ABC transporter, substrate bin...	26	72	
gi	30020491	ref	NP_832122.1	hypothetical protein [Bacillus...	26	72	
gi	21244445	ref	NP_644027.1	conserved hypothetical protein...	26	72	
gi	15226030	ref	NP_179099.1	retroelement pol polyprotein -...	26	72	
gi	28901509	ref	NP_801164.1	putative ferrichrome ABC trans...	26	72	
gi	15901437	ref	NP_346041.1	conserved hypothetical protein...	26	72	
gi	23307111	dbj	BAC16541.1	ferric vibrioferrin transport s...	26	72	
gi	30157001	ref	XP_291865.2	similar to olfactory receptor ...	25	97	L
gi	17506261	ref	NP_491002.1	Amino acid permease family mem...	25	97	L
gi	21224537	ref	NP_630316.1	putative permease [Streptomyce...	25	97	
gi	30018841	ref	NP_830472.1	Multidrug resistance protein B...	25	97	
gi	15611696	ref	NP_223347.1	putative TYPE II DNA MODIFICAT...	25	97	
gi	15217347	gb	AAK92685.1	AC090714_18 putative retrotranspo...	25	97	
gi	630612	pir	S44629	F22B7.10 protein - Caenorhabditis ele...	25	97	
gi	16944534	emb	CAD11330.1	hypothetical protein [Neurospor...	25	97	



gi 26251614 gb AAN84835.1	Hypothetical protein C55C2.5c [C...	25	97	
gi 1477386 gb AAC37338.1	This CDS feature is included to s...	25	97	
gi 24666563 ref NP_649079.2	CG6836-PA [Drosophila melanoga...	25	97	L
gi 17506263 ref NP_491003.1	Amino acid permease family mem...	25	97	L
gi 17861760 gb AAL39357.1	GH26215p [Drosophila melanogaster]	25	97	L
gi 17555266 ref NP_497282.1	Putative membrane protein, wit...	25	97	L
gi 26336525 dbj BAC31945.1	unnamed protein product [Mus mu...	25	97	L
gi 21231138 ref NP_637055.1	MFS transporter [Xanthomonas c...	25	97	
gi 30840221 emb CAD61285.1	fertility restorer [Raphanus sa...	25	97	
gi 17552842 ref NP_498909.1	DumPY : shorter than wild-type...	25	97	L
gi 21398624 ref NP_654609.1	sugar_tr, Sugar (and other) tr...	25	97	
gi 28564962 gb AAO32565.1	FKS1 [Saccharomyces kluyveri]	25	130	
gi 3914053 sp O13396 MSH2 NEUCR	DNA mismatch repair protein...	25	130	
gi 20837204 ref XP_158536.1	hypothetical protein XP_158536...	25	130	L
gi 29349732 ref NP_813235.1	conserved hypothetical protein...	25	130	
gi 23273294 gb AAH34950.1	TANK-binding kinase 1 [Homo sapi...	25	130	L
gi 19923703 ref NP_037056.2	CD44 antigen; Cell surface gly...	25	130	L
gi 7019547 ref NP_037386.1	TANK-binding kinase 1; NF-kB-ac...	25	130	L
gi 26991318 ref NP_746743.1	conserved hypothetical protein...	25	130	
gi 15791673 ref NP_281496.1	hypothetical protein Cj0305c [...	25	130	
gi 21595149 gb AAH32196.1	Unknown (protein for MGC:38244) ...	25	130	
gi 30022512 ref NP_834143.1	ABC transporter ATP-binding pr...	25	130	
gi 29377576 ref NP_816730.1	serine/threonine protein kinas...	25	130	
gi 27706584 ref XP_242294.1	hypothetical protein XP_242294...	25	130	L
gi 28521689 ref XP_288504.1	hypothetical protein XP_288504...	25	130	L
gi 22957373 gb ZP_00005078.1	hypothetical protein [Rhodoba...	25	130	
gi 17543364 ref NP_501353.1	Putative nuclear protein, with...	25	130	L
gi 21402483 ref NP_658468.1	ABC_tran, ABC transporter [Bac...	25	130	
gi 27368877 emb CAD59596.1	MRP-like ABC transporter [Oryza...	25	130	
gi 27718495 ref XP_216902.1	similar to TANK-binding kinase...	25	130	L
gi 21397994 ref NP_653979.1	hypothetical protein predicted...	24	174	
gi 15800733 ref NP_286747.1	unknown [Escherichia coli O157...	24	174	
gi 17456139 ref XP_051362.2	similar to Transmembrane 6 sup...	24	174	L
gi 84991 pir A20647	heat shock protein 22 - fruit fly (Dro...	24	174	L
gi 13473381 ref NP_104948.1	hypothetical protein [Mesorhiz...	24	174	
gi 17569347 ref NP_510111.1	Putative endoplasmic reticulum...	24	174	L
gi 27666390 ref XP_221376.1	similar to hypothetical protei...	24	174	L
gi 631889 pir C48213	syntaxin 2 - rat	24	174	
gi 27707330 ref XP_242328.1	hypothetical protein XP_242328...	24	174	L
gi 15830651 ref NP_309424.1	hypothetical protein [Escheric...	24	174	
gi 13124733 sp P02515 HS22 DROME	Heat shock protein 22	24	174	

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|20909630|ref|XP\_153478.1| hypothetical protein XP\_153478 [Mus musculus]  
Length = 197

Score = 29.9 bits (63), Expect = 3.8  
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 4 WPFHFAF 10

WPFHFAF

Sbjct: 12 WPFHFAF 18

☐ >gi|19113394|ref|NP\_596602.1| SNF2 family dna repair protein by similarity [Schi pombe]  
gi|7492644|pir|T39936 probable helicase - fission yeast (Schizosaccharomyces pom

gi|3116120|emb|CAA18870.1| zinc finger protein; zf-C3HC4 type (RING finger); SNF2  
 helicase; DEAD box helicase; putative DNA repair protein  
 [Schizosaccharomyces pombe]  
 Length = 1040

Score = 29.9 bits (63), Expect = 3.8  
 Identities = 11/16 (68%), Positives = 12/16 (75%), Gaps = 1/16 (6%)

Query: 13 QILATIAMSHCRPTVY 28  
 +IL IA SH RPTVY  
 Sbjct: 458 EILTKIAPSH-RPTVY 472

☐ >gi|27685447|ref|XP\_217453.1| serine (or cysteine) proteinase inhibitor, clade  
 [Rattus norvegicus]  
 Length = 398

Score = 29.5 bits (62), Expect = 5.1  
 Identities = 12/27 (44%), Positives = 15/27 (55%), Gaps = 8/27 (29%)

Query: 4 WPFHFAFFHQILATIAMSHCRPTVYKQ 30  
 W HF FF IL T+ +S +VY Q  
 Sbjct: 3 W--HFPFF--ILTTVTLS----SVYSQ 21

☐ >gi|121111|sp|P07092|GDN RAT Glia derived nexin precursor (GDN) (Protease nexin  
gi|92273|pir|B27496 proteinase inhibitor nexin 1 precursor - rat (fragment)  
gi|204284|gb|AAA41209.1| GDN precursor  
 Length = 397

Score = 29.5 bits (62), Expect = 5.1  
 Identities = 12/27 (44%), Positives = 15/27 (55%), Gaps = 8/27 (29%)

Query: 4 WPFHFAFFHQILATIAMSHCRPTVYKQ 30  
 W HF FF IL T+ +S +VY Q  
 Sbjct: 3 W--HFPFF--ILTTVTLS----SVYSQ 21

☐ >gi|21287767|gb|EAA00088.1| ENSANGP00000017962 [Anopheles gambiae str. PEST]  
 Length = 314

Score = 29.1 bits (61), Expect = 6.9  
 Identities = 19/47 (40%), Positives = 22/47 (46%), Gaps = 20/47 (42%)

Query: 4 WPFHFAFFH---Q-----ILA--TI--AMSHCRPTVYKQTSII 34  
 WP+H A FH Q IL TI A SHC VY Q+ +I  
 Sbjct: 52 WPHVALFHRKDAQEYACGGSILDENTILTA-SHC---VYTQSGVI 94

☐ >gi|25148238|ref|NP\_499962.2| Protein kinase family member (42.4 kD) [Caenorhabd  
gi|17976530|gb|AAC24403.2| Hypothetical protein K11H12.9 [Caenorhabditis elegans]  
 Length = 376

Score = 28.6 bits (60), Expect = 9.2  
 Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 12 HQILATIAMSH 22  
 HQILA +AM H  
 Sbjct: 203 HQILAAVAMMH 213

☐ >gi|7505805|pir|T34435 hypothetical protein K11H12.9 - Caenorhabditis elegans  
 Length = 374

Score = 28.6 bits (60), Expect = 9.2  
 Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 12 HQILATIAMSH 22  
 HQILA +AM H

Sbjct: 201 HQILAAVAMMH 211

☐ >[gi|27695175|ref|XP\\_223369.1|](#) similar to low density lipoprotein receptor-related low density lipoprotein-related protein 4; Low Density Lipoprotein Receptor Related Protein 4; corin [Mus musculus] [Rattus norvegicus]  
Length = 276

Score = 28.2 bits (59), Expect = 12  
Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 6 FHFAFFHQIL 15

FHF+ FHQ+L

Sbjct: 2 FHFSLFHQVL 11

☐ >[gi|17558564|ref|NP\\_506763.1|](#) Predicted CDS, putative plasma membrane member, with at least 5 transmembrane domains, nematode specific [Caenorhabditis elegans]  
[gi|7497294|pir|T19886](#) hypothetical protein C41G6.7 - Caenorhabditis elegans  
Length = 405

Score = 28.2 bits (59), Expect = 12  
Identities = 13/23 (56%), Positives = 15/23 (65%), Gaps = 4/23 (17%)

Query: 13 QILATIAMS-HCRPTVYKQTSII 34

IL +I MS HCR TV K SI+

Sbjct: 350 HILVSIMSSHCRDTV-K--SIV 369

☐ >[gi|30145805|emb|CAB02832.2|](#) C. elegans SRW-24 protein (corresponding sequence C [Caenorhabditis elegans])  
Length = 418

Score = 28.2 bits (59), Expect = 12  
Identities = 13/23 (56%), Positives = 15/23 (65%), Gaps = 4/23 (17%)

Query: 13 QILATIAMS-HCRPTVYKQTSII 34

IL +I MS HCR TV K SI+

Sbjct: 363 HILVSIMSSHCRDTV-K--SIV 382

☐ >[gi|630666|pir|S40748](#) hypothetical protein F54C8.6 - Caenorhabditis elegans  
Length = 309

Score = 27.8 bits (58), Expect = 17  
Identities = 11/22 (50%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 7 HFA--FFHQI-----LATIA 19

HF FFHQI +ATIA

Sbjct: 223 HFVVQFFHQIIHLILSSIATIA 244

☐ >[gi|17555608|ref|NP\\_498145.1|](#) Predicted CDS, putative membrane protein family m least 4 transmembrane domains, nematode specific [Caenorhabditis elegans]  
[gi|7331800|gb|AAF60488.1|](#) Hypothetical protein Y32H12A.1 [Caenorhabditis elegans]  
Length = 310

Score = 27.8 bits (58), Expect = 17  
Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 11 FHQILATIAMS 21

FHQILA + MS

Sbjct: 47 FHQILAIVLMS 57

☐ >[gi|17553568|ref|NP\\_499077.1|](#) Predicted CDS, putative membrane protein, with a domain, nematode specific [Caenorhabditis elegans]

gi|20141894|sp|P34444|YL86 CAEEL Hypothetical protein F54C8.6 in chromosome III  
gi|15718117|emb|CAA80158.2| Hypothetical protein F54C8.6 [Caenorhabditis elegans]  
 Length = 265

Score = 27.8 bits (58), Expect = 17  
 Identities = 11/22 (50%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 7 HFA--FFHQI-----LATIA 19  
 HF FFHQI +ATIA  
 Sbjct: 223 HFVVQFFHQIIHLILSSIATIA 244

☐ >gi|25342678|pir|B88555 protein F54C8.6 [imported] - Caenorhabditis elegans  
 Length = 306

Score = 27.8 bits (58), Expect = 17  
 Identities = 11/22 (50%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 7 HFA--FFHQI-----LATIA 19  
 HF FFHQI +ATIA  
 Sbjct: 264 HFVVQFFHQIIHLILSSIATIA 285

☐ >gi|21245069|ref|NP\_644651.1| conserved hypothetical protein [Xanthomonas axonop  
 str. 306]  
gi|21110802|gb|AAM39187.1| conserved hypothetical protein [Xanthomonas axonopodis  
 str. 306]  
 Length = 129

Score = 27.4 bits (57), Expect = 22  
 Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 3 KWPFHFFAFF 11  
 KW F FAFF  
 Sbjct: 12 KWQFRFAFF 20

☐ >gi|24374681|ref|NP\_718724.1| DnaJ domain protein [Shewanella oneidensis MR-1]  
gi|24349326|gb|AAN56168.1|AE015754.2 DnaJ domain protein [Shewanella oneidensis M  
 Length = 402

Score = 26.9 bits (56), Expect = 30  
 Identities = 9/11 (81%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 6 FHFAFFHQILA 16  
 FH AFF QILA  
 Sbjct: 170 FH-AFFEQILA 179

☐ >gi|10946860|ref|NP\_067441.1| TATA box binding protein (Tbp)-associated factor,  
 A [Mus musculus]  
gi|1842204|emb|CAA71091.1| TAFI48 protein [Mus musculus]  
 Length = 453

Score = 26.9 bits (56), Expect = 30  
 Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 4 WP-FHFFAFF 11  
 WP FHF+FF  
 Sbjct: 380 WPAFHFSFF 388

☐ >gi|27672343|ref|XP\_221755.1| similar to hypothetical protein MGC2408 [Homo sap  
 norvegicus]  
 Length = 256

Score = 26.9 bits (56), Expect = 30  
 Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 2/16 (12%)

Query: 1 PYKWPF-HFAFFHQIL 15  
 PY+W F FAFFH +L  
 Sbjct: 130 PYEW-FGDFFAFFHALL 144

☐ >gi|28871387|ref|NP\_794006.1| hypothetical protein [Pseudomonas syringae pv. tom  
 gi|28854638|gb|AA057701.1| hypothetical protein [Pseudomonas syringae pv. tomato  
 Length = 1111

Score = 26.9 bits (56), Expect = 30  
 Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 8 FAFFHQIL 15  
 FAFFHQ+L  
 Sbjct: 728 FAFFHQLL 735

☐ >gi|20094540|ref|NP\_614387.1| Uncharacterized membrane protein specific for M.ka  
 family [Methanopyrus kandleri AV19]  
 gi|19887659|gb|AAM02317.1| Uncharacterized membrane protein specific for M.kandle  
 family [Methanopyrus kandleri AV19]  
 Length = 244

Score = 26.9 bits (56), Expect = 30  
 Identities = 10/22 (45%), Positives = 11/22 (50%), Gaps = 8/22 (36%)

Query: 4 WPFHFAFFHQILA-----TIAM 20  
 W FAFF Q+L TI M  
 Sbjct: 27 W---FAFFPQVLTFGLWLTIVM 45

☐ >gi|9632199|ref|NP\_048911.1| a555R [Paramecium bursaria Chlorella virus 1]  
 gi|7461690|pir|T18057 hypothetical protein a555R - Chlorella virus PBCV-1  
 gi|2447141|gb|AAC96999.1| a555R [Paramecium bursaria Chlorella virus 1]  
 Length = 113

Score = 26.9 bits (56), Expect = 30  
 Identities = 10/16 (62%), Positives = 10/16 (62%), Gaps = 4/16 (25%)

Query: 14 ILATIA--MSHC--RP 25  
 IL TI MSHC RP  
 Sbjct: 60 ILETIVFIMSHCYKRP 75

☐ >gi|15078968|ref|NP\_149719.1| 256R [Invertebrate iridescent virus 6]  
 gi|15042337|gb|AAK82117.1|AF303741 256 256R [Chilo iridescent virus]  
 Length = 78

Score = 26.5 bits (55), Expect = 40  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 YKWPFHFHAF 10  
 ++W FHFHAF  
 Sbjct: 39 FRWSFHFHAF 47

☐ >gi|30177923|gb|EAA45104.1| ENSANGP00000023294 [Anopheles gambiae str. PEST]  
 Length = 232

Score = 26.5 bits (55), Expect = 40  
 Identities = 15/36 (41%), Positives = 16/36 (44%), Gaps = 17/36 (47%)

Query: 4 WPFHFAFFHQ-----IL--ATI--AMSHC 23  
 WP+H A FHQ IL TI A SHC  
 Sbjct: 1 WPWHAAlFHQDKKHKEYACGGsILDETTILTA-SHC 35

☐ >gi|15641102|ref|NP\_230734.1| periplasmic binding protein-related protein [Vibri  
 gi|11345643|pir|A82245 periplasmic binding protein-related protein VC1089 [impor  
 Vibrio cholerae (strain N16961 serogroup O1)

gi|9655557|gb|AAF94248.1| periplasmic binding protein-related protein [Vibrio cho  
Length = 270

Score = 26.5 bits (55), Expect = 40  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 5 PFHF~~A~~FFHQ 13

P+H+ FFHQ

Sbjct: 80 PYHYTFFHQ 88

☐ >gi|19114288|ref|NP\_593376.1| hypothetical protein [Schizosaccharomyces pombe]  
gi|3219957|sp|P87136|YDM5 SCHPO Hypothetical protein C57A7.05 in chromosome I  
gi|7491179|pir|T38949 hypothetical protein SPAC57A7.05 - fission yeast  
(Schizosaccharomyces pombe)  
gi|2104440|emb|CAB08763.1| hypothetical protein; similar to S. cerevisiae YDL231C  
contains 11 predicted transmembrane helices;  
leucine-serine rich [Schizosaccharomyces pombe]  
Length = 1337

Score = 26.5 bits (55), Expect = 40  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 3 KWPFHF 8

KWPFHF

Sbjct: 1308 KWPFHF 1313

☐ >gi|22293495|emb|CAD31853.1| putative chemosensory receptor 7 [Heliothis viresce  
Length = 397

Score = 26.1 bits (54), Expect = 54  
Identities = 10/17 (58%), Positives = 11/17 (64%), Gaps = 5/17 (29%)

Query: 1 PY--K-WPFHF~~A~~FFHQI 14

PY K WPF A+ HQI

Sbjct: 174 PYELKYWPF--AYIHQI 188

☐ >gi|17230565|ref|NP\_487113.1| probable glycosyl transferase [Nostoc sp. PCC 7120  
gi|25530026|pir|AB2190 hypothetical protein alr3073 [imported] - Nostoc sp. (str  
7120)  
gi|17132167|dbj|BAB74772.1| ORF\_ID:alr3073-probable glycosyl transferase [Nostoc  
Length = 324

Score = 26.1 bits (54), Expect = 54  
Identities = 9/18 (50%), Positives = 9/18 (50%), Gaps = 8/18 (44%)

Query: 2 YKWPF---HFAFFHQIL 15

YKWPF HQIL

Sbjct: 185 YKWPFVVVKQ---HQIL 198

☐ >gi|19552310|ref|NP\_600312.1| hypothetical membrane protein [Corynebacterium glu  
13032]  
gi|21323851|dbj|BAB98477.1| Hypothetical membrane protein [Corynebacterium glutam  
13032]  
Length = 241

Score = 26.1 bits (54), Expect = 54  
Identities = 10/19 (52%), Positives = 13/19 (68%), Gaps = 4/19 (21%)

Query: 4 WPFHF--AFFHQILATIAM 20

WPFHF A +I+A IA+

Sbjct: 71 WPFHFSDAL--RIIAAIAL 87

☐ >gi|22982800|ref|ZP\_00028030.1| hypothetical protein [Burkholderia fungorum]  
Length = 294

Score = 26.1 bits (54), Expect = 54  
Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 3/16 (18%)

Query: 13 QILATIAMSHCR--PT 26  
+ILATI +HCR PT  
Sbjct: 51 EILATI-RTHCRTVPT 65

☐ >gi|14521448|ref|NP\_126924.1| CARBON STARVATION PROTEIN A. [Pyrococcus abyssi]  
gi|7444677|pir|E75032 carbon starvation protein A homolog PAB1554 [similarity] -  
Pyrococcus abyssi (strain Orsay)  
gi|5458667|emb|CAB50154.1| cstA carbon starvation protein A [Pyrococcus abyssi]  
Length = 592

Score = 26.1 bits (54), Expect = 54  
Identities = 10/19 (52%), Positives = 13/19 (68%), Gaps = 5/19 (26%)

Query: 4 WPFHFAF--FHQILATIAM 20  
WP AF +Q+LA+IAM  
Sbjct: 493 WP---AFSGMNQMLASIAM 508

☐ >gi|17544706|ref|NP\_501719.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family memb  
elegans]  
gi|7510956|pir|T27720 hypothetical protein ZK1251.3 - Caenorhabditis elegans  
gi|3881515|emb|CAA92499.1| Hypothetical protein ZK1251.3 [Caenorhabditis elegans]  
Length = 253

Score = 26.1 bits (54), Expect = 54  
Identities = 11/18 (61%), Positives = 11/18 (61%), Gaps = 5/18 (27%)

Query: 8 FAFFHQI---LATIAMSH 22  
FAFF I LA AMSH  
Sbjct: 214 FAFF--IVCNLAPRAMSH 229

☐ >gi|7510844|pir|T29765 hypothetical protein ZC581.4 - Caenorhabditis elegans  
Length = 209

Score = 26.1 bits (54), Expect = 54  
Identities = 9/15 (60%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query: 5 PFHF--AFFHQ--IL 15  
PFHF FF Q IL  
Sbjct: 57 PFHFPQTFFQQPHIL 71

☐ >gi|15235511|ref|NP\_195444.1| ATPase, E1-E2 type family [Arabidopsis thaliana]  
gi|12643808|sp|Q9M3H5|AHM1 ARATH Potential cadmium/zinc-transporting ATPase HMA1  
gi|25407802|pir|D85440 Cu2+-transporting ATPase-like protein [imported] - Arabid  
thaliana  
gi|4006855|emb|CAB16773.1| Cu2+-transporting ATPase-like protein [Arabidopsis tha  
gi|7270710|emb|CAB80393.1| Cu2+-transporting ATPase-like protein [Arabidopsis tha  
Length = 819

Score = 26.1 bits (54), Expect = 54  
Identities = 11/27 (40%), Positives = 14/27 (51%), Gaps = 11/27 (40%)

Query: 2 YKWPFHFAFFHQILATIAMSHCRPTVY 28  
+KWPF L+T A CR +VY  
Sbjct: 385 FKWPF-----LSTAA---CRGSVY 400

☐ >gi|5579428|gb|AAD45549.1|U70376 14 SpcE [Streptomyces netropsis]  
Length = 427

Score = 26.1 bits (54), Expect = 54  
Identities = 10/15 (66%), Positives = 11/15 (73%), Gaps = 3/15 (20%)

Query: 6 FH--FAFFHQ-ILAT 17  
 FH FAF HQ +LAT  
 Sbjct: 391 FHTCFAFLHQALLAT 405

☐ >gi|7710954|emb|CAB90352.1| putative metal ATPase [Arabidopsis thaliana]  
 Length = 819

Score = 26.1 bits (54), Expect = 54  
 Identities = 11/27 (40%), Positives = 14/27 (51%), Gaps = 11/27 (40%)

Query: 2 YKWPFFHFAFFHQILATIAMSHCRPTVY 28  
 +KWPF L+T A CR +VY  
 Sbjct: 385 FKWPF-----LSTAA---CRGSVY 400

☐ >gi|15606525|ref|NP\_213905.1| NADH dehydrogenase I chain M [Aquifex aeolicus]  
 gi|7432313|pir|B70414 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoM  
 Aquifex aeolicus  
 gi|2983743|gb|AAC07304.1| NADH dehydrogenase I chain M [Aquifex aeolicus VF5]  
 Length = 491

Score = 26.1 bits (54), Expect = 54  
 Identities = 11/19 (57%), Positives = 12/19 (63%), Gaps = 3/19 (15%)

Query: 1 PYKWPFFHFAFFHQILATIA 19  
 PY F FAFF +LA IA  
 Sbjct: 370 PY---FTFAFFLAVLAGIA 385

Score = 19.7 bits (39), Expect = 4415  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 4 WPFH 7  
 WPFH  
 Sbjct: 226 WPFH 229

☐ >gi|21242454|ref|NP\_642036.1| MFS transporter [Xanthomonas axonopodis pv. citri]  
 gi|21107899|gb|AAM36572.1| MFS transporter [Xanthomonas axonopodis pv. citri str.  
 Length = 474

Score = 25.7 bits (53), Expect = 72  
 Identities = 10/17 (58%), Positives = 12/17 (70%), Gaps = 2/17 (11%)

Query: 6 FHFAFFHQILA--TIAM 20  
 F FAFF Q LA T+A+  
 Sbjct: 167 FAFAFFVQFLAVPTVAL 183

☐ >gi|28917410|gb|EAA27114.1| hypothetical protein [Neurospora crassa]  
 Length = 620

Score = 25.7 bits (53), Expect = 72  
 Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 1 PYKWPFFH 8  
 PYKW F F  
 Sbjct: 36 PYKWTFQF 43

☐ >gi|23612355|ref|NP\_703935.1| transportin [Plasmodium falciparum 3D7]  
 gi|23498596|emb|CAD50547.1| transportin [Plasmodium falciparum 3D7]  
 Length = 1147

Score = 25.7 bits (53), Expect = 72  
 Identities = 7/8 (87%), Positives = 7/8 (87%)